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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/052,817

DATE: 02/12/2002  
 TIME: 15:35:44

Input Set : A:\seqlist\_0609 4460005.txt  
 Output Set: N:\CRF3\02122002\J052817.raw

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7 <110> APPLICANT: Tanzi, Rudolph E.  
 10 Kovacs, Dora  
 13 Saunders, Aleister J.  
 19 <120> TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods  
 for  
 22 Alzheimer's Disease  
 27 <130> FILE REFERENCE: 0609.4460005  
 C--> 33 <140> CURRENT APPLICATION NUMBER: US/10/052,817  
 C--> 36 <141> CURRENT FILING DATE: 2002-01-23  
 41 <150> PRIOR APPLICATION NUMBER: 09/241,606  
 44 <151> PRIOR FILING DATE: 1999-02-02  
 48 <150> PRIOR APPLICATION NUMBER: 09/148,503  
 51 <151> PRIOR FILING DATE: 1998-09-04  
 55 <150> PRIOR APPLICATION NUMBER: 60/093,297  
 58 <151> PRIOR FILING DATE: 1998-07-17  
 63 <160> NUMBER OF SEQ ID NOS: 27  
 69 <170> SOFTWARE: PatentIn Ver. 2.0  
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 78 <211> LENGTH: 4577  
 81 <212> TYPE: DNA  
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 96 <222> LOCATION: (44)..(112)  
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 132 Met Gly Lys Asn  
 135 -20  
 146 aaa ctc ctt cat cca agt ctg gtt ctt ctc ctc ttg gtc ctc ctg ccc 103  
 149 Lys Leu Leu His Pro Ser Leu Val Leu Leu Leu Val Leu Leu Pro  
 152 -15 -10 -5  
 158 aca gac gcc tca gtc tct gga aaa ccg cag tat atg gtt ctg gtc ccc 151  
 161 Thr Asp Ala Ser Val Ser Gly Lys Pro Gln Tyr Met Val Leu Val Pro  
 164 -1 1 5 10  
 170 tcc ctg ctc cac act gag acc act gag aag ggc tgt gtc ctt ctg agc 199  
 173 Ser Leu Leu His Thr Glu Thr Thr Glu Lys Gly Cys Val Leu Leu Ser  
 176 15 20 25  
 182 tac ctg aat gag aca gtg act gta agt gct tcc ttg gag tct gtc agg 247

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188 30 35 40 45
194 gga aac agg agc ctc ttc act gac ctg gag gcg gag aat gac gta ctc 295
197 Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu Asn Asp Val Leu
200 50 55 60
206 cac tgt gtc gcc ttc gct gtc cca aag tct tca tcc aat gag gag gta 343
209 His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Ser Asn Glu Glu Val
212 65 70 75
218 atg ttc ctc act gtc caa gtg aaa gga cca acc caa gaa ttt aag aag 391
221 Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln Glu Phe Lys Lys
224 80 85 90
230 cgg acc aca gtg atg gtt aag aac gag gac agt ctg gtc ttt gtc cag 439
233 Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu Val Phe Val Gln
236 95 100 105
242 aca gac aaa tca atc tac aaa cca ggg cag aca gtg aaa ttt cgt gtt 487
245 Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val Lys Phe Arg Val
248 110 115 120 125
254 gtc tcc atg gat gaa aac ttt cac ccc ctg aat gag ttg att cca cta 535
257 Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu Leu Ile Pro Leu
260 130 135 140
268 gta tac att cag gat ccc aaa gga aat cgc atc gca caa tgg cag agt 583
271 Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala Gln Trp Gln Ser
274 145 150 155
280 ttc cag tta gag ggt ggc ctc aag caa ttt tct ttt ccc ctc tca tca 631
283 Phe Gln Leu Glu Gly Gly Leu Lys Gln Phe Ser Phe Pro Leu Ser Ser
286 160 165 170
292 gag ccc ttc cag ggc tcc tac aag gtg gtg gta cag aag aaa tca ggt 679
295 Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Val Gln Lys Lys Ser Gly
298 175 180 185
304 gga agg aca gag cac cct ttc acc gtg gag gaa ttt gtt ctt ccc aag 727
307 Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe Val Leu Pro Lys
310 190 195 200 205
316 ttt gaa gta caa gta aca gtg cca aag ata atc acc atc ttg gaa gaa 775
319 Phe Glu Val Gln Val Thr Val Pro Lys Ile Ile Thr Ile Leu Glu Glu
322 210 215 220
328 gag atg aat gta tca gtg tgt ggc cta tac aca tat ggg aag cct gtc 823
331 Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr Gly Lys Pro Val
334 225 230 235
340 cct gga cat gtg act gtg agc att tgc aga aag tat agt gac gct tcc 871
343 Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr Ser Asp Ala Ser
346 240 245 250
352 gac tgc cac ggt gaa gat tca cag gct ttc tgt gag aaa ttc agt gga 919
355 Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu Lys Phe Ser Gly
358 255 260 265
364 cag cta aac agc cat ggc tgc ttc tat cag caa gta aaa acc aag gtc 967
367 Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val Lys Thr Lys Val
370 270 275 280 285
376 ttc cag ctg aag agg aag gag tat gaa atg aaa ctt cac act gag gcc 1015
379 Phe Gln Leu Lys Arg Lys Glu Tyr Glu Met Lys Leu His Thr Glu Ala

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382          290          295          300
389 cag atc caa gaa gaa gga aca gtg gtg gaa ttg act gga agg cag tcc 1063
392 Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr Gly Arg Gln Ser
395          305          310          315
401 agt gaa atc aca aga acc ata acc aaa ctc tca ttt gtg aaa gtg gac 1111
404 Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe Val Lys Val Asp
407          320          325          330
413 tca cac ttt cga cag gga att ccc ttc ttt ggg cag gtg cgc cta gta 1159
416 Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln Val Arg Leu Val
419          335          340          345
425 gat ggg aaa ggc gtc cct ata cca aat aaa gtc ata ttc atc aga gga 1207
428 Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile Phe Ile Arg Gly
431 350          355          360          365
437 aat gaa gca aac tat tac tcc aat gct acc acg gat gag cat ggc ctt 1255
440 Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp Glu His Gly Leu
443          370          375          380
449 gta cag ttc tct atc aac acc acc aac gtt atg ggt acc tct ctt act 1303
452 Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly Thr Ser Leu Thr
455          385          390          395
461 gtt agg gtc aat tac aag gat cgt agt ccc tgt tac ggc tac cag tgg 1351
464 Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr Gly Tyr Gln Trp
467          400          405          410
473 gtg tca gaa gaa cac gaa gag gca cat cac act gct tat ctt gtg ttc 1399
476 Val Ser Glu Glu His Glu Glu Ala His His Thr Ala Tyr Leu Val Phe
479          415          420          425
485 tcc cca agc aag agc ttt gtc cac ctt gag ccc atg tct cat gaa cta 1447
488 Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met Ser His Glu Leu
491 430          435          440          445
497 ccc tgt ggc cat act cag aca gtc cag gca cat tat att ctg aat gga 1495
500 Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr Ile Leu Asn Gly
503          450          455          460
509 ggc acc ctg ctg ggg ctg aag aag ctc tcc ttt tat tat ctg ata atg 1543
512 Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr Tyr Leu Ile Met
515          465          470          475
521 gca aag gga ggc att gtc cga act ggg act cat gga ctg ctt gtg aag 1591
524 Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly Leu Leu Val Lys
527          480          485          490
533 cag gaa gac atg aag ggc cat ttt tcc atc tca atc cct gtg aag tca 1639
536 Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile Pro Val Lys Ser
539          495          500          505
545 gac att gct cct gtc gct cgg ttg ctc atc tat gct gtt tta cct acc 1687
548 Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr
551 510          515          520          525
557 ggg gac gtg att ggg gat tct gca aaa tat gat gtt gaa aat tgt ctg 1735
560 Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu
563          530          535          540
569 gcc aac aag gtg gat ttg agc ttc agc cca tca caa agt ctc cca gcc 1783
572 Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala
575          545          550          555

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581 tca cac gcc cac ctg cga gtc aca gcg gct cct cag tcc gtc tgc gcc 1831
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593 ctc cgt gct gtg gac caa agc gtg ctg ctc atg aag cct gat gct gag 1879
596 Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys Pro Asp Ala Glu
599          575          580          585
605 ctc tcg gcg tcc tcg gtt tac aac ctg cta cca gaa aag gac ctc act 1927
608 Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr
611 590          595          600          605
617 ggc ttc cct ggg cct ttg aat gac cag gac gat gaa gac tgc atc aat 1975
620 Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn
623          610          615          620
629 cgt cat aat gtc tat att aat gga atc aca tat act cca gta tca agt 2023
632 Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser
635          625          630          635
641 aca aat gaa aag gat atg tac agc ttc cta gag gac atg ggc tta aag 2071
644 Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys
647          640          645          650
653 gca ttc acc aac tca aag att cgt aaa ccc aaa atg tgt cca cag ctt 2119
656 Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met Cys Pro Gln Leu
659          655          660          665
665 caa cag tat gaa atg cat gga cct gaa ggt cta cgt gta ggt ttt tat 2167
668 Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr
671 670          675          680          685
677 gag tca gat gta atg gga aga ggc cat gca cgc ctg gtg cat gtt gaa 2215
680 Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu Val His Val Glu
683          690          695          700
689 gag cct cac acg gag acc gta cga aag tac ttc cct gag aca tgg atc 2263
692 Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile
695          705          710          715
701 tgg gat ttg gtg gtg gta aac tca gca ggg gtg gct gag gta gga gta 2311
704 Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala Glu Val Gly Val
707          720          725          730
713 aca gtc cct gac acc atc acc gag tgg aag gca ggg gcc ttc tgc ctg 2359
716 Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu
719          735          740          745
725 tct gaa gat gct gga ctt ggt atc tct tcc act gcc tct ctc cga gcc 2407
728 Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala
731 750          755          760          765
737 ttc cag ccc ttc ttt gtg gag ctt aca atg cct tac tct gtg att cgt 2455
740 Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg
743          770          775          780
749 gga gag gcc ttc aca ctc aag gcc acg gtc cta aac tac ctt ccc aaa 2503
752 Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys
755          785          790          795
761 tgc atc cgg gtc agt gtg cag ctg gaa gcc tct ccc gcc ttc ctt gct 2551
764 Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala
767          800          805          810
773 gtc cca gtg gag aag gaa caa gcg cct cac tgc atc tgt gca aac ggg 2599

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776	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	
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785	cgg	caa	act	gtg	tcc	tgg	gca	gta	acc	cca	aag	tca	tta	gga	aat	gtg	2647
788	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	
791	830					835					840					845	
797	aat	ttc	act	gtg	agc	gca	gag	gca	cta	gag	tct	caa	gag	ctg	tgt	ggg	2695
800	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	
803					850					855					860		
809	act	gag	gtg	cct	tca	gtt	cct	gaa	cac	gga	agg	aaa	gac	aca	gtc	atc	2743
812	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	
815				865					870					875			
821	aag	cct	ctg	ttg	gtt	gaa	cct	gaa	gga	cta	gag	aag	gaa	aca	aca	ttc	2791
824	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	
827			880					885					890				
833	aac	tcc	cta	ctt	tgt	cca	tca	ggt	ggt	gag	gtt	tct	gaa	gaa	tta	tcc	2839
836	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	
839		895					900					905					
845	ctg	aaa	ctg	cca	cca	aat	gtg	gta	gaa	gaa	tct	gcc	cga	gct	tct	gtc	2887
848	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	
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857	tca	gtt	ttg	gga	gac	ata	tta	ggc	tct	gcc	atg	caa	aac	aca	caa	aat	2935
860	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	
863				930					935						940		
869	ctt	ctc	cag	atg	ccc	tat	ggc	tgt	gga	gag	cag	aat	atg	gtc	ctc	ttt	2983
872	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	
875			945						950					955			
881	gct	cct	aac	atc	tat	gta	ctg	gat	tat	cta	aat	gaa	aca	cag	cag	ctt	3031
884	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	
887			960				965						970				
893	act	cca	gag	atc	aag	tcc	aag	gcc	att	ggc	tat	ctc	aac	act	ggt	tac	3079
896	Thr	Pro	Glu	Ile	Lys	Ser	Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	
899		975				980						985					
905	cag	aga	cag	ttg	aac	tac	aaa	cac	tat	gat	ggc	tcc	tac	agc	acc	ttt	3127
908	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	
911	990					995				1000						1005	
917	ggg	gag	cga	tat	ggc	agg	aac	cag	ggc	aac	acc	tgg	ctc	aca	gcc	ttt	3175
920	Gly	Glu	Arg	Tyr	Gly	Arg	Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	
923			1010						1015					1020			
929	gtt	ctg	aag	act	ttt	gcc	caa	gct	cga	gcc	tac	atc	ttc	atc	gat	gaa	3223
932	Val	Leu	Lys	Thr	Phe	Ala	Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	
935			1025						1030				1035				
941	gca	cac	att	acc	caa	gcc	ctc	ata	tgg	ctc	tcc	cag	agg	cag	aag	gac	3271
944	Ala	His	Ile	Thr	Gln	Ala	Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	
947		1040					1045					1050					
953	aat	ggc	tgt	ttc	agg	agc	tct	ggg	tca	ctg	ctc	aac	aat	gcc	ata	aag	3319
956	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	
959	1055					1060					1065						
965	gga	gga	gta	gaa	gat	gaa	gtg	acc	ctc	tcc	gcc	tat	atc	acc	atc	gcc	3367
968	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	

VERIFICATION SUMMARY

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L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date